

Amendments to the Specification

Please replace the paragraph beginning at p. 4, ln. 5 with the following paragraph:

The stereostructure of decarbamylase and similar enzymes has not been determined. It has been found from sequence similarity analysis for proteins, whose amino acid sequences had already been known, using a protein sequence database, PIR Release57 (National Center for Biotechnology Information (NCBI)) that decarbamylase has a weak sequence similarity of about 25-30% to hydrolase, such as amidase and nitrilase. However, none of the stereostructures of these enzymes having weak sequence similarity have been determined. Therefore, it is practically impossible to estimate the stereostructure of decarbamylase by a so-called homology modeling technique using the stereostructures of similar proteins, which is often used for the molecular design technique (e.g., Swiss-Pdbviewer (modeling program) (Swiss Institute of Bioinformatics (SIB), ExPASy Molecular Biology Server (~~available from~~ <http://www.expasy.ch/>)); Guex, N. and Peitsch, M.C. (1997) SWISS-MODEL and the Swiss-PdbViewer: An environment for comparative protein modeling, *Electrophoresis* 18, 2714-2723). Even if the stereostructure of a similar enzyme is determined, it is difficult to obtain, based on a sequence similarity of less than 30%, the stereostructure model of decarbamylase with a sufficient accuracy for application of a reasonable molecular design method. The accurate atomic coordinate data of decarbamylase is required to predict amino acid mutations involved in a change in the optimum pH of an enzyme reaction, an improvement in specific activity, and the like with high precision for the purpose of molecular design. If the stereostructure of decarbamylase can be determined, precise analysis of the stereostructure and a reasonable molecular design technique based thereon can be conducted, thereby further making it possible to rapidly or efficiently obtain a modified enzyme which is advantageous in industrial applications.